SEQUENCE LISTING

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OKUDA, MITSUYOSHI

SAEKI, KATSUHISA

KUBOTA, HIROMI

HITOMI, JUN

KAGEYAMA, YASUSHI

SHIKATA, SHITSUW

NOMURA, MASAFUMI


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<150> PCT/JP98/04528

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Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Xaa Xaa Gly
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Phe Ser Lys Gln Xaa Gln Thr Gly Ala Ala Ala Phe Leu Val Glu Ser
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Glu Asn Val Lys Leu Xaa Lys Gly Leu Xaa Lys Lys Leu Glu Thr Val
65                  70                  75                  80

Pro Ala Asn Asn Lys Leu His Ile Xaa Gln Phe Asn Gly Pro Ile Leu
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Glu Glu Thr Lys Gln Xaa Leu Glu Xaa Thr Gly Ala Lys Ile Leu Asp
                100                 105                 110

Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val Xaa
        115                 120                 125

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Val Xaa Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp Val
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Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
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            245             250             255

Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly
            260             265             270

His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Xaa Thr Asn
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Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp
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Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu
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Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr
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Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr
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Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Xaa Ile
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Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala Asn
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His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr Pro
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Ser Ser Xaa Leu Ser Thr Ser Gln Lys Ala Thr Tyr Xaa Phe Thr Ala
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Pro Xaa Xaa Xaa Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe
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Gly Phe Ser Lys Gln Xaa Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
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Ser Glu Asn Val Lys Leu Xaa Lys Gly Leu Xaa Lys Lys Leu Glu Thr
65                  70                  75                  80

Val Pro Ala Asn Asn Lys Leu His Ile Xaa Gln Phe Asn Gly Pro Ile
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Leu Glu Glu Thr Lys Gln Xaa Leu Glu Xaa Thr Gly Ala Lys Ile Leu
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Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
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Asp Ser Xaa Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
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Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
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Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
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Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Xaa
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Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
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        115                 120                 125

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aga gga atc act cct aag cct tcc cta ttg aaa gca gct ttg att gca        1488
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                 485             490             495

ggt gct gct gat gtt gga ttg ggt tat ccg aac gga aac caa gga tgg        1536
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Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr Phe Thr Ala
         530             535             540

acg gcg ggc aag cca ttg aaa atc tcc ctg gta tgg tcg gat gcc cct        1680
Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala Pro
545             550             555             560
```

```
gca agc act act gct tct gta acc ctg gtc aat gat ttg gat ttg gtc      1728
Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val
                565              570              575

att aca gca cca aac gga aca aga tat gtc ggg aat gac ttc tca gca      1776
Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp Phe Ser Ala
                580              585              590

cca ttt gac aat aac tgg gat ggc cgc aat aac gta gaa aat gta ttt      1824
Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe
                595              600              605

att aat tcg ccc caa agt gga aca tat acc att gag gtg caa gca tat      1872
Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr
            610              615              620

aat gtg ccg gtt gga cca caa aac ttc tcg ttg gca att gtg aac taa      1920
Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn
625              630              635
```

<210> 4

<211> 639

<212> PRT

<213> Bacillus sp.

<400> 4

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Met Arg Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala Ile
1                   5                   10                  15

Leu Ser Thr Val Ala Leu Asn Asn Pro Ser Ala Gly Asp Ala Arg Thr
                20                  25                  30

Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Val Ser Gly
        35                  40                  45

Phe Ser Lys Gln Arg Gln Thr Gly Ala Ala Ala Phe Leu Val Glu Ser
    50                  55                  60

Glu Asn Val Lys Leu Leu Lys Gly Leu Leu Lys Lys Leu Glu Thr Val
65                  70                  75                  80

Pro Ala Asn Asn Lys Leu His Ile Val Gln Phe Asn Gly Pro Ile Leu
                85                  90                  95

Glu Glu Thr Lys Gln Lys Leu Glu Thr Thr Gly Ala Lys Ile Leu Asp
            100                 105                 110
```

Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val Gln
    115                 120                 125

Ser Lys Val Arg Ser Ile Glu His Val Glu Ser Val Glu Pro Tyr Leu
    130                 135                 140

Pro Lys Tyr Lys Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser Thr
145                 150                 155                 160

Leu Val Lys Ala Leu Ala Leu Asp Thr Lys Gln Asn Asn Lys Glu Val
                165                 170                 175

Gln Leu Arg Gly Ile Glu Glu Ile Ala Gln Tyr Val Ala Ser Asn Asp
                180                 185                 190

Val His Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp Val
        195                 200                 205

Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
    210                 215                 220

Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp Thr
225                 230                 235                 240

Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile Thr
                245                 250                 255

Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly
        260                 265                 270

His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ala Thr Asn
    275                 280                 285

Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp
    290                 295                 300

Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu Phe
305                 310                 315                 320

Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp Gly
                325                 330                 335

Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp Asp
        340                 345                 350

```
Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu
    355                 360             365

Arg Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn Ala
    370             375             380

Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr
385             390             395             400

Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr
            405             410             415

Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Tyr Ile
            420             425             430

Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala Asn
        435             440             445

His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr Pro
    450             455             460

Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys Asn
465             470             475             480

Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile Ala
                485             490             495

Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly Trp
        500             505             510

Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn Glu
    515             520             525

Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr Phe Thr Ala
    530             535             540

Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala Pro
545             550             555             560

Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val
            565             570             575

Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp Phe Ser Ala
        580             585             590
```

```
Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe
    595                 600                 605

Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr
    610                 615                 620

Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn
625                 630                 635
```

<210> 5

<211> 1923

<212> DNA

<213> Bacillus sp.


<220>

<221> CDS

<222> (1)..(1923)


<400> 5

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atg aga aag aag aaa aag gtg ttt tta tct gtt tta tca gct gca gcg        48
Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala
1                5                  10                 15

att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt gca agg        96
Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg
            20                 25                 30

aat ttt gat ctg gat ttc aaa gga att cag aca aca act gat gct aaa       144
Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
            35                 40                 45

ggt ttc tcc aag cag ggg cag act ggt gct gct gct ttt ctg gtg gaa       192
Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
    50                 55                 60

tct gaa aat gtg aaa ctc cca aaa ggt ttg cag aag aag ctt gaa aca       240
Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
65                 70                 75                 80

gtc ccg gca aat aat aaa ctc cat att atc caa ttc aat gga cca att       288
Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
                85                 90                 95

tta gaa gaa aca aaa cag cag ctg gaa aaa aca ggg gca aag att ctc       336
Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
            100                105                110
```

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```
gac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt      384
Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
        115                 120                 125

aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat      432
Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
    130                 135                 140

ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca      480
Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
145                 150                 155                 160

gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag      528
Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
                165                 170                 175

gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat      576
Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
                180                 185                 190

gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat      624
Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
        195                 200                 205

gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg      672
Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
    210                 215                 220

ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat      720
Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
225                 230                 235                 240

aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att      768
Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
                245                 250                 255

act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat      816
Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
                260                 265                 270

ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act      864
Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
        275                 280                 285

aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg      912
Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
    290                 295                 300

gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta      960
Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
305                 310                 315                 320

ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg     1008
Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
                325                 330                 335

gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat     1056
Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
        340                 345                 350
```

```
gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat        1104
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
        355             360             365

gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat        1152
Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
370             375             380

gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct        1200
Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
385             390             395             400

tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg        1248
Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
                405             410             415

aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc        1296
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
            420             425             430

ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg        1344
Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
        435             440             445

aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca        1392
Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
450             455             460

ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa        1440
Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
465             470             475             480

aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att        1488
Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
                485             490             495

gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga        1536
Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
            500             505             510

tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac        1584
Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
            515             520             525

gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act        1632
Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
530             535             540

gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc        1680
Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
545             550             555             560

cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt        1728
Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
                565             570             575

gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act        1776
Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
            580             585             590
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```
tcg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta     1824
Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
        595             600             605

ttt att aat gca cca caa agc ggg acg tat aca att gag gta cag gct     1872
Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
    610             615             620

tat aac gta ccg gtt gga cca cag acc ttc tcg ttg gca att gtg aat     1920
Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile Val Asn
625             630             635             640

taa                                                                 1923


<210>   6

<211>   640

<212>   PRT

<213>   Bacillus sp.


<400>   6

Met Arg Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala
1               5               10              15

Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg
            20              25              30

Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
    35              40              45

Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
    50              55              60

Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
65              70              75              80

Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
            85              90              95

Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
        100             105             110

Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
    115             120             125
```

-32-

```
Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
    130             135             140

Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
145             150             155             160

Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
            165             170             175

Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
        180             185             190

Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
    195             200             205

Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
    210             215             220

Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
225             230             235             240

Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
            245             250             255

Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
        260             265             270

Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
    275             280             285

Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
290             295             300

Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
305             310             315             320

Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
            325             330             335

Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
        340             345             350

Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
    355             360             365
```

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Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
    370             375             380

Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
385             390             395             400

Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
            405             410             415

Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
        420             425             430

Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
    435             440             445

Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
    450             455             460

Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
465             470             475             480

Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
            485             490             495

Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
        500             505             510

Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
    515             520             525

Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
    530             535             540

Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
545             550             555             560

Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
            565             570             575

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
        580             585             590

Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
    595             600             605

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```
Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
    610             615             620

Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile Val Asn
625             630             635             640


<210>  7

<211>  1923

<212>  DNA

<213>  Bacillus sp.


<220>

<221>  CDS

<222>  (1)..(1923)



<400>  7
atg aga aag aag aaa aag gtg ttt tta tct gtt tta tca gct gca gcg       48
Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala
1               5                   10                  15

att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt gca agg       96
Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg
                20                  25                  30

aat ttt gat ctg gat ttc aaa gga att cag aca aca act gat gct aaa      144
Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
        35                  40                  45

ggt ttc tcc aag cag ggg cag act ggt gct gct gct ttt ctg gtg gaa      192
Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
    50                  55                  60

tct gaa aat gtg aaa ctc cca aaa ggt ttg cag aag aag ctt gaa aca      240
Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
65                  70                  75                  80

gtc ccg gca aat aat aaa ctc cat att atc caa ttc aat gga cca att      288
Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
                85                  90                  95

tta gaa gaa aca aaa cag cag ctg gaa aaa aca ggg gca aag att ctc      336
Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
                100                 105                 110

gac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt      384
Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
        115                 120                 125
```

-35-

```
aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat       432
Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
    130                 135                 140

ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca       480
Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
145                 150                 155                 160

gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag       528
Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
                165                 170                 175

gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat       576
Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
                180                 185                 190

gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat       624
Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
            195                 200                 205

gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg       672
Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
    210                 215                 220

ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat       720
Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
225                 230                 235                 240

aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att       768
Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
                245                 250                 255

act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat       816
Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
            260                 265                 270

ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act       864
Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
    275                 280                 285

aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg       912
Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
    290                 295                 300

gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta       960
Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
305                 310                 315                 320

ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg      1008
Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
                325                 330                 335

gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat      1056
Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
            340                 345                 350

gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat      1104
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
            355                 360                 365
```

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gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat          1152
Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
    370             375             380

gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct          1200
Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
385             390             395             400

tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg          1248
Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
                405             410             415

aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc          1296
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
            420             425             430

ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg          1344
Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
            435             440             445

aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca          1392
Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
    450             455             460

ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa          1440
Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
465             470             475             480

aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att          1488
Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
            485             490             495

gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga          1536
Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
            500             505             510

tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac          1584
Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
    515             520             525

gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act          1632
Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
    530             535             540

gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc          1680
Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
545             550             555             560

cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt          1728
Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
            565             570             575

gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act          1776
Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
            580             585             590

tcg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta          1824
Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
    595             600             605

-37-

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:tt att aat gca cca caa agc ggg acg tat aca att gaa gta cag gct       1872
⁾he Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
    610             615             620

:at aac gta ccg gtt gga cca cag aac ttc tcg ttg gca att gtg aat       1920
ᴸyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn
⁵25             630             635             640

taa                                                                   1923


<210>   8

<211>   640

<212>   PRT

<213>   Bacillus sp.


<400>   8

Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala
1               5               10              15


Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg
            20              25              30


Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
    35              40              45


Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
    50              55              60


Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
65              70              75              80


Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
            85              90              95


Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
            100             105             110


Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
        115             120             125


Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
    130             135             140
```

-38-

```
Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
145             150         155             160

Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
            165             170             175

Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
            180             185             190

Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
            195             200             205

Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
    210             215             220

Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
225             230             235             240

Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
            245             250             255

Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
            260             265             270

Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
    275             280             285

Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
    290             295             300

Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
305             310             315             320

Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
            325             330             335

Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
            340             345             350

Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
    355             360             365

Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
    370             375             380
```

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Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
385                 390                 395                 400

Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
                    405                 410                 415

Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
            420                 425                 430

Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
            435                 440                 445

Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
    450                 455                 460

Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
465                 470                 475                 480

Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
                    485                 490                 495

Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
            500                 505                 510

Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
        515                 520                 525

Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
    530                 535                 540

Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
545                 550                 555                 560

Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
                565                 570                 575

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
            580                 585                 590

Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
        595                 600                 605

Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
    610                 615                 620

-40-

Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn
625                 630             635                 640

<210>  9

<211>  20

<212>  PRT

<213>  Bacillus sp.


<400>  9

Asn Asp Val Ala Arg His Ile Val Lys Ala Asp Val Ala Gln Ser Ser
1               5                   10                  15

Tyr Gly Leu Tyr
            20

<210>  10

<211>  14

<212>  PRT

<213>  Bacillus sp.


<400>  10

Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
1               5                   10

<210>  11

<211>  13

<212>  PRT

<213>  Bacillus sp.


<400>  11

Ile Lys Pro Asp Val Met Ala Pro Gly Thr Tyr Ile Leu
1               5                   10

<210>  12

<211>  20

<212>  PRT

<213>  Bacillus sp.

<400> 12

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly
1               5                   10                  15

Ser Tyr Ala Asp
            20

<210> 13

<211> 16

<212> PRT

<213> Bacillus sp.


<400> 13

Lys Asn Asp Met Val Ile Leu Phe Ala Ala Gly Asn Glu Gly Pro Asn
1               5                   10                  15

<210> 14

<211> 24

<212> DNA

<213> Artificial/Unknown


<220>

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<222> ()..()

<223> Description of Artificial Sequence: primer


<220>

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<222> (6)..(6)

<223> n is a, g, c or t

<220>

<221> misc_feature

<222> (12)..(12)

<223> n is a, g, c or t


<220>

<221> misc_feature

<222> (18)..(18)

<223> n is a, g, c or t


<220>

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<222> (21)..(21)

<223> n is a, g, c or t


<400> 14
athgtnaarg cngaygtngc ncar                                    24

<210> 15

<211> 23

<212> DNA

<213> Artificial/Unknown


<220>

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<222> ()..()

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (9)..(9)

<223> n is a, g, c or t


<220>

<221> misc_feature

<222> (15)..(15)

<223> n is a, g, c or t

<220>

<221> misc_feature

<222> (21)..(21)

<223> n is a, g, c or t

<400> 15
tadttyggnc trcantaccg ngg                                        23

<210> 16

<211> 23

<212> DNA

<213> Artificial/Unknown


<220>

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<222> ()..()

<223> Description of Artificial Sequence: primer

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<222> (9)..(9)

<223> n is a, g, c or t


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<223> n is a, g, c or t


<220> misc_feature

<221> misc_feature

<222> (21)..(21)

<223> n is a, g, c or t


<400> 16
athaarccng aygtnatggc ncc                                                23

<210> 17

<211> 24

<212> DNA

<213> Artificial/Unknown


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<223> Description of Artificial Sequence: primer

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<223> n is a, g, c or t

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<223> n is a, g, c or t

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<223> n is a, g, c or t

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<222> (18)..(18)

<223> n is a, g, c or t

<220>

<221> misc_feature

<222> (21)..(21)

<223> n is a, g, c or t

<220>

<221> misc_feature

<222> (24)..(24)

<223> n is a, g, c or t

<400> 17
ttrcgntadt gncanccncg ntgn                                                      24

<210> 18

<211> 23

<212> DNA

<213> Artificial/Unknown

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<222> ()..()

<223> Description of Artificial Sequence: primer

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<222> (6)..(6)

<223> n is a, g, c or t

<220>

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<222> (9)..(9)

<223> n is a, g, c or t


<220>

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<222> (12)..(12)

<223> n is a, g, c or t


<220>

<221> misc_feature

<222> (15)..(15)

<223> n is a, g, c or t


<220>

<221> misc_feature

<222> (18)..(18)

<223> n is a, g, c or t


<400> 18
athacngtng gngcnacnga raa                                                    23


<210> 19

<211> 23

<212> DNA

<213> Artificial/Unknown


<220>

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<222> ()..()

<223> Description of Artificial Sequence: primer


<220>

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<222> (12)..(12)

<223> n is a, g, c or t


<220>

<221> misc_feature

<222> (18)..(18)

<223> n is a, g, c or t


<400> 19
ttrctrtacc antadranaa rcg                                                23


<210> 20

<211> 23

<212> DNA

<213> Artificial/Unknown


<220>

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<222> ()..()

<223> Description of Artificial Sequence: primer

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<222> (12)..(12)

<223> n is a, g, c or t


<220>

<221> misc_feature

<222> (18)..(18)

<223> n is a, g, c or t


<400> 20
aaygayatgg tnatgytntt ygc                                              23

<210> 21

<211> 21

<212> DNA

<213> Artificial/Unknown

<220>

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<222> ()..()

<223> Description of Artificial Sequence: primer


<400> 21
tcggcaactg cgacaatctg g                                                21

<210> 22

<211> 21

<212> DNA

-50-

<213> Artificial/Unknown

<220>

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<222> ()..()

<223> Description of Artificial Sequence: primer


<400> 22
tctggaatct gtcgtgtagg c                                                    21

<210> 23

<211> 20

<212> DNA

<213> Artificial/Unknown


<220>

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<222> ()..()

<223> Description of Artificial Sequence: primer


<400> 23
aacggcggta ccatcagtgc                                                      20

<210> 24

<211> 21

<212> DNA

<213> Artificial/Unknown


<220>

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<222> ()..()

<223> Description of Artificial Sequence: primer

<400> 24
ggaggcttgc cttccaatct g                                                    21

SEQUENCE LISTING

<110>    KAO CORPORATION


<120>    Alkaline Protease


<130>    FP-KS-0498


<150>    JP 09-274570
<151>    1997-10-07


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<210>    1
<211>    639
<212>    PRT
<213>    *Bacillus sp.*


<220>

<221>    misc_feature

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         148, 160, 165, 172, 183, 187, 188, 189, 194, 286, 306, 324, 369, 431, 501,
         531, 541, 584, 591, 592, 594, 595, 596, 611, 632

<223>    Xaa=arbitraty amino acid


<400>

Met Arg Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala Ile
1               5                   10                  15

Leu Ser Thr Val Ala Leu Xaa Asn Pro Ser Ala Gly Xaa Ala Arg Xaa
            20                  25                  30

Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Xaa Xaa Gly
        35                  40                  45

Phe Ser Lys Gln Xaa Gln Thr Gly Ala Ala Ala Phe Leu Val Glu Ser
    50                  55                  60

Glu Asn Val Lys Leu Xaa Lys Gly Leu Xaa Lys Lys Leu Glu Thr Val
65                  70                  75                  80

Pro Ala Asn Asn Lys Leu His Ile Xaa Gln Phe Asn Gly Pro Ile Leu
                85                  90                  95

Glu Glu Thr Lys Gln Xaa Leu Glu Xaa Thr Gly Ala Lys Ile Leu Asp
                100                 105                 110

Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val Xaa
                115                 120                 125

Ser Xaa Xaa Xaa Xaa Ile Glu His Val Glu Ser Val Glu Pro Tyr Leu
    130                 135                 140

Pro Xaa Tyr Xaa Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser Xaa
145                 150                 155                 160

Leu Val Lys Ala Xaa Ala Leu Asp Thr Lys Gln Xaa Asn Lys Glu Val
                165                 170                 175

Gln Leu Arg Gly Ile Glu Xaa Ile Ala Gln Xaa Xaa Xaa Ser Asn Asp
                180                 185                 190

Val Xaa Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp Val
                195                 200                 205

2 / 2 3

Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
    210             215            220

Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp Thr
225             230            235            240

Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile Thr
          245            250            255

Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly
          260            265            270

His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Xaa Thr Asn
          275            280            285

Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp
          290            295            300

Ser Xaa Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu Phe
305             310            315            320

Ser Gln Ala Xaa Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp Gly
          325            330            335

Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp Asp
          340            345            350

Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu
          355            360            365

Xaa Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn Ala
          370            375            380

Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr
385             390            395            400

Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr
          405            410            415

Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Xaa Ile
            420                 425                 430

Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala Asn
            435                 440                 445

His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr Pro
            450                 455                 460

Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys Asn
465                 470                 475                 480

Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile Ala
            485                 490                 495

Gly Ala Ala Asp Xaa Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly Trp
            500                 505               - 510

Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn Glu
            515                 520                 525

Ser Ser Xaa Leu Ser Thr Ser Gln Lys Ala Thr Tyr Xaa Phe Thr Ala
            530                 535                 540

Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala Pro
545                 550                 555                 560

Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val
            565                 570                 575

Ile Thr Ala Pro Asn Gly Thr Xaa Tyr Val Gly Asn Asp Phe Xaa Xaa
            580                 585                 590

Pro Xaa Xaa Xaa Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe
            595                 600                 605

Ile Asn Xaa Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr
            610                 615                 620

Asn Val Pro Val Gly Pro Gln Xaa Phe Ser Leu Ala Ile Val Asn

625                 630                 635

<210>   2

<211>   640

<212>   PRT

<213>   *Bacillus sp.*


<220>

<221>   misc_feature

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        149, 161, 166, 173, 184, 188, 189, 190, 195, 287, 307, 325, 370, 432, 502,
        532, 542, 585, 592, 593, 595, 596, 597, 612, 633

<223>   Xaa=arbitrary amino acid


<400>

Met Arg Xaa Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala

1               5                   10                  15

Ile Leu Ser Thr Val Ala Leu Xaa Asn Pro Ser Ala Gly Xaa Ala Arg

            20                  25                  30

Xaa Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Xaa Xaa

            35                  40                  45

Gly Phe Ser Lys Gln Xaa Gln Thr Gly Ala Ala Ala Phe Leu Val Glu

        50                  55                  60

Ser Glu Asn Val Lys Leu Xaa Lys Gly Leu Xaa Lys Lys Leu Glu Thr

65                  70                  75                  80

Val Pro Ala Asn Asn Lys Leu His Ile Xaa Gln Phe Asn Gly Pro Ile

5 / 2 3

Leu Glu Glu Thr Lys Gln Xaa Leu Glu Xaa Thr Gly Ala Lys Ile Leu

                100                   105                   110

Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val

                115                   120                   125

Xaa Ser Xaa Xaa Xaa Xaa Ile Glu His Val Glu Ser Val Glu Pro Tyr

            130                   135                   140

Leu Pro Xaa Tyr Xaa Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser

145                   150                   155                   160

Xaa Leu Val Lys Ala Xaa Ala Leu Asp Thr Lys Gln Xaa Asn Lys Glu

                165                   170            ·      175

Val Gln Leu Arg Gly Ile Glu Xaa Ile Ala Gln Xaa Xaa Xaa Ser Asn

                180                   185                   190

Asp Val Xaa Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp

                195                   200                   205

Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly

            210                   215                   220

Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp

225                   230                   235                   240

Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile

                245                   250                   255

Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn

                260                   265                   270

Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Xaa Thr

                275                   280                   285

Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met

```
                290                   295                   300
Asp Ser Xaa Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
305                   310                   315                   320
Phe Ser Gln Ala Xaa Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
                    325                   330                   335
Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
                340                   345                   350
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
                355                   360                   365
Glu Xaa Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
                370                   375                   380   .
Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
385                   390                   395                   400
Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
                    405                   410                   415
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Xaa
                420                   425                   430
Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
                435                   440                   445
Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
                450                   455                   460
Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
465                   470                    475                   480 .
Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
                485                   490                   495
Ala Gly Ala Ala.Asp Xaa Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
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```
                500                 505                 510
Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
            515                 520                 525
Glu Ser Ser Xaa Leu Ser Thr Ser Gln Lys Ala Thr Tyr Xaa Phe Thr
        530                 535                 540
Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
    545                 550                 555                 560
Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
                565                 570                 575
Val Ile Thr Ala Pro Asn Gly Thr Xaa Tyr Val Gly Asn Asp Phe Xaa
            580                 585                 590
Xaa Pro Xaa Xaa Xaa Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
                595                 600                 605
Phe Ile Asn Xaa Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
            610                 615                 620
Tyr Asn Val Pro Val Gly Pro Gln Xaa Phe Ser Leu Ala Ile Val Asn
    625                 630                 635                 640
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<210> 3

<211> 1920

<212> DNA

<213> *Bacillus sp.*


<400>

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atg aga aag aag aag gtg ttt tta tct gtt tta tca gct gca gcg att    48
Met Arg Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala Ile
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      1            5                10                15
ctg tcg act gtt gca tta aac aat ccc tcg gct ggt gat gca agg act   96
Leu Ser Thr Val Ala Leu Asn Asn Pro Ser Ala Gly Asp Ala Arg Thr
                   20                25                30
ttt gat ctg gat ttt aaa gga att caa aca aca acc gat gtc agt ggt   144
Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Val Ser Gly
          35                40                45
ttc tcc aaa cag cga caa aca ggt gcg gct gca ttt ctg gtg gag tct   192
Phe Ser Lys Gln Arg Gln Thr Gly Ala Ala Ala Phe Leu Val Glu Ser
          50                55                60
gaa aat gtg aaa ctt ctt aaa gga ttg cta aag aaa ctt gaa aca gta   240
Glu Asn Val Lys Leu Leu Lys Gly Leu Leu Lys Lys Leu Glu Thr Val
65                70                75                80
ccg gca aat aat aaa ctc cat att gtc caa ttc aat ggc ccc att tta   288
Pro Ala Asn Asn Lys Leu His Ile Val Gln Phe Asn Gly Pro Ile Leu
                   85                90                95
gaa gaa aca aaa cag aag cta gag aca act gga gca aag att ctc gac   336
Glu Glu Thr Lys Gln Lys Leu Glu Thr Thr Gly Ala Lys Ile Leu Asp
                   100               105               110
tac atc cct gat tat gca tat att gtc gag tat gag ggg gat gtt cag   384
Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val Gln
                   115               120               125
tca aaa gtc cgc tcc att gaa cac gtg gaa tca gtg gag cca tac ttg   432
Ser Lys Val Arg Ser Ile Glu His Val Glu Ser Val Glu Pro Tyr Leu
          130               135               140
ccg aaa tac aaa ata gat ccc cag ctt ttc aca aaa ggc gca tcg acg   480
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Pro Lys Tyr Lys Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser Thr

145            150            155      -     160

ctg gtg aaa gcg ttg gcg ctt gat acg aag cag aac aat aaa gaa gtg    528

Leu Val Lys Ala Leu Ala Leu Asp Thr Lys Gln Asn Asn Lys Glu Val

           165           170           175

caa tta aga ggc atc gag gaa atc gct cag tac gta gca agc aat gac    576

Gln Leu Arg Gly Ile Glu Glu Ile Ala Gln Tyr Val Ala Ser Asn Asp

           180           185           190

gtc cat tat att acg gca aag cct gaa tat aag gtg atg aat gat gtg    624

Val His Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp Val

           195           200           205

gcc aga ggt att gtc aaa gcg gat gtg gca cag agc agc tac ggt ttg    672

Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu

   210            215           220

tat gga caa ggc cag att gtc gca gtt gcc gat act gga ttg gat aca    720

Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp Thr

225            230            235         240

gga aga aac gac agt tcg atg cat gaa gcc ttc cgc ggt aaa ata aca    768

Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile Thr

           245           250           255

gca cta tat gca ctg ggt cgg acg aat aat gcg aat gat acg aac ggt    816

Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly

           260           265           270

cat ggt acc cat gtg gca ggt tcg gta tta gga aat ggc gca acg aat    864

His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ala Thr Asn

           275           280           285

aaa gga atg gca cct caa gcg aat ctg gtt ttt caa tcc atc atg gat 912
Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp
        290                 295                 300

agc agt ggt ggg ctt gga ggc ttg cct tcc aat ctg caa acc tta ttc 960
Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu Phe
305                 310                 315                 320

agc caa gca ttc agt gca ggt gcc aga att cat aca aac tcc tgg ggg 1008
Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp Gly
                    325                 330                 335

gca gcg gtg aat ggg gcc tac acg aca gat tcc aga aat gtg gat gac 1056
Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp Asp
                    340                 345                 350

tat gta agg aaa aat gat atg acg att ctt ttc gcg gct ggg aat gaa 1104
Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu
                355                 360                 365

agg ccg aac ggc ggt acc atc agt gca cct ggt acg gct aaa aac gcc 1152
Arg Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn Ala
        370                 375                 380

ata aca gtc ggc gca acc gaa aac ctg cgt cca agc ttc ggt tcc tat 1200
Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr
385                 390                 395                 400

gca gat aat att aac cac gtt gca cag ttc tct tcc cgt ggc ccg aca 1248
Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr
                    405                 410                 415

aaa gat ggg cga atc aag cct gat gtc atg gcg cca ggg aca tac att 1296
Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Tyr Ile

tta tca gca aga tct tct ctt gca ccc gat tcc tcc ttc tgg gcg aat 1344
Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala Asn

          435                  440                  445

cat gac agc aaa tat gcc tat atg ggt gga acg tcc atg gca aca ccg 1392
His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr Pro

    450                  455                  460

att gtt gcg ggg aat gtt gca cag ctc cgt gag cat ttt gtg aaa aat 1440
Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys Asn

465               470                  475                  480

aga gga atc act cct aag cct tcc cta ttg aaa gca gct ttg att gca 1488
Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile Ala

             485                  490                  495

ggt gct gct gat gtt gga ttg ggt tat ccg aac gga aac caa gga tgg 1536
Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly Trp

          500                  505                  510

ggc cga gtg acc ctg gat aaa tcg ttg aac gtt gcc tat gtg aac gaa 1584
Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn Glu

          515                  520                  525

tcc agt gcc cta tca act agc caa aaa gcg aca tat acc ttt act gca 1632
Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr Phe Thr Ala

          530                  535                  540

acg gcg ggc aag cca ttg aaa atc tcc ctg gta tgg tcg gat gcc cct 1680
Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala Pro

545               550                  555                  560

gca agc act act gct tct gta acc ctg gtc aat gat ttg gat ttg gtc 1728

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Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val
            565                 570                 575

att aca gca cca aac gga aca aga tat gtc ggg aat gac ttc tca gca 1776
Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp Phe Ser Ala
            580                 585                 590

cca ttt gac aat aac tgg gat ggc cgc aat aac gta gaa aat gta ttt 1824
Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe
            595                 600                 605

att aat tcg ccc caa agt gga aca tat acc att gag gtg caa gca tat 1872
Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr
        610                 615                 620

aat gtg ccg gtt gga cca caa aac ttc tcg ttg gca att gtg aac taa 1920
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625                 630                 635
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<211>    1923

<212>    DNA

<213>    *Bacillus sp.*


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1                5                  10                 15

att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt gca agg    96
Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg
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                20                      25                      30
aat ttt gat ctg gat ttc aaa gga att cag aca aca act gat gct aaa  144
Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
            35                      40                      45
ggt ttc tcc aag cag ggg cag act ggt gct gct gct ttt ctg gtg gaa  192
Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
        50                      55                      60
tct gaa aat gtg aaa ctc cca aaa ggt ttg cag aag aag ctt gaa aca  240
Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
65                      70                      75                      80
gtc ccg gca aat aat aaa ctc cat att atc caa ttc aat gga cca att  288
Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
                85                      90                      95
tta gaa gaa aca aaa cag cag ctg gaa aaa aca ggg gca aag att ctc  336
Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
            100                     105                     110
gac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt  384
Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
            115                     120                     125
aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat  432
Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
        130                     135                     140
ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca  480
Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
145                     150                     155                     160
gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag  528
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Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
          165             170             175

gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat 576
Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
          180             185             190

gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat 624
Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
          195             200             205

gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg 672
Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
          210             215             220

ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat 720
Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
225              230             235            240

aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att 768
Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
          245             250             255

act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat 816
Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
          260             265             270

ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act 864
Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
          275             280             285

aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg 912
Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
          290             295             300

gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta 960
Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
305              310              315              320

ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg 1008
Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
                 325              330              335

gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat 1056
Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
              340              345              350

gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat 1104
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
              355              360              365

gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat 1152
Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
     370              375              380

gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct 1200
Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
385              390              395              400

tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg 1248
Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
                 405              410              415

aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc 1296
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
              420              425              430

ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg 1344
Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala

435                    440                    445

aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca 1392
Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
        450                    455                    460

ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa 1440
Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
465                    470                    475                    480

aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att 1488
Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
                        485                    490                    495

gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga 1536
Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
                    500                    505                    510

tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac 1584
Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
                515                    520                    525

gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act 1632
Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
            530                    535                    540

gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc 1680
Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
545                    550                    555                    560

cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt 1728
Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
                565                    570                    575

gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act 1776

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
           580           585           590

tcg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta 1824
Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
           595           600           605

ttt att aat gca cca caa agc ggg acg tat aca att gag gta cag gct 1872
Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
         610           615           620

tat aac gta ccg gtt gga cca cag acc ttc tcg ttg gca att gtg aat 1920
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625           630           635     ·      640

taa                                            1923


<210> 5

<211> 1923

<212> DNA

<212> *Bacillus sp.*


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Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala
           5           10           15

att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt gca agg   96
Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg
         20           25           30

aat ttt gat ctg gat ttc aaa gga att cag aca aca act gat gct aaa 144

Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
        35                  40                  45

ggt ttc tcc aag cag ggg cag act ggt gct gct gct ttt ctg gtg gaa  192
Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
        50                  55                  60

tct gaa aat gtg aaa ctc cca aaa ggt ttg cag aag aag ctt gaa aca  240
Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
65                  70                  75                  80

gtc ccg gca aat aat aaa ctc cat att atc caa ttc aat gga cca att  288
Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
                85                  90          .       95

tta gaa gaa aca aaa cag cag ctg gaa aaa aca ggg gca aag att ctc  336
Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
                100                 105                 110

gac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt  384
Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
                115                 120                 125

aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat  432
Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
                130                 135                 140

ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca  480
Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
145                 150                 155                 160

gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag  528
Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
                165                 170                 175

gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat  576
Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
            180             185             190

gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat  624
Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
            195             200             205

gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg  672
Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
            210             215             220

ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat  720
Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
225             230             235             240

aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att  768
Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
            245             250             255

act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat  816
Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
            260             265             270

ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act  864
Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
            275             280             285

aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg  912
Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
            290             295             300

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Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu

ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg 1008
Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp

                       325                    330                    335

gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat 1056
Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp

                  340                    345                    350

gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat 1104
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn

             355                    360                    365

gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat 1152
Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn

        370                    375                    380

gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct 1200
Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser

385                    390                    395                    400

tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg 1248
Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro

                  405                    410                    415

aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc 1296
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe

             420                    425                    430

ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg 1344
Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala

        435                    440                    445

aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca 1392

Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
450             455             460

ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa 1440
Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
465             470             475             480

aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att 1488
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                485             490             495

gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga 1536
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                500             505           · 510

tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac 1584
Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
                515             520             525

gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act 1632
Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
530             535             540

gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc 1680
Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
545             550             555             560

cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt 1728
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gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act 1776
Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
                580             585             590

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Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
        595              600              605

ttt att aat gca cca caa agc ggg acg tat aca att gaa gta cag gct 1872
Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
     610              615              620

tat aac gta ccg gtt gga cca cag aac ttc tcg ttg gca att gtg aat 1920
Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn
625              630              635              640

taa                                                            1923
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